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GenCore version 5.1.6
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using sw model protein search, OM protein earch time 60 Seconds (without alignments) 1582.266 Million cell updates/sec May 11, 2004, 16:41:19; Search Run on:

US-10-650-369-12 1715 1 MVVKVGINGFGRIGRLAFRR.....EMSYTAQLVRTLEYFAKIAK Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

1586107 seqs, 282547505 residues Searched:

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1586107 hits satisfying chosen parameters: ų O Total number

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

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Database

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1: geneseqp1980s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AAM50665 RESULT

AAM50665 standard; protein; 336 AA

AAM50665;

(first entry) 08-APR-2002 Streptococcus dysgalactiae gapC plasmin binding protein DysGapC.

DysGapC; GapC; plasmin binding protein; epitope; infection; vaccine; immunisation; mastitis; therapy.

Streptococcus dysgalactiae.

WO200196379-A2.

20-DEC-2001.

11-JUN-2001; 2001WO-CA000836

12-JUN-2000; 2000US-0211247P.

(UYSA-) UNIV SASKATCHEWAN.

Fontaine M;

Ď,

Perez-Casal

Potter AA,

2002-098051/13. N-PSDB; ABA91328 WPI:

Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in parauberis, vertebrates

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Claim 8; Fig 1A-B; 116pp; English.

The present sequence is that of the GapC plasmin binding protein, bysGapC, of Streptococcus dysgalactiae ATCC 43078, an isolate from a case of bovine mastitis. The invention relates to novel GapC multiple epitope fusion proteins that comprise epitopes from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae, Streptococcus parauberis, Streptococcus uberis and Streptococcus iniae (see AAM50665-69). A claimed example is PolyGap4 (see AAM50664). Expression vectors and host cells for production of the multiple epitope fusion proteins are provided. The multiple epitope proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in

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S.uberis, S.parauberis, or S.iniae, useful as vaccine component for
treating streptococcal infection which causes mastitis in vertebrates.
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claimed methods of detecting Streptococcus antibodies. The mult epitope proteins are capable of eliciting broad immunity agains variety of streptococcal infections while minimising the number antigens present in the final formulation and concomitantly reconduction costs
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Pred. No. 8.6e-145;
Mismatches 0;
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                                                                      Sequence 336 AA;
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The present sequence is that of the GapC plasmin binding protein (DysGalGapC) of Streptococcus dysgalactiae ATCC 43078, a clinical isolate from bovine mastitis. It is encoded by the GapC gene given in ABA91248. GapC protein, which has no signal sequence or membrane anchor domain, is capable of eliciting an immune response in a vertebrate. The invention provides the GapC genes and proteins of 5 Streptococcus species, as well as recombinant vectors, host cells and vaccine compositions comprising GapC polynucleotides or proteins. The vaccines are used to treat or prevent a bacterial infection, especially a streptococcal infection, and mastitis in particular (claimed). GapC proteins are also used in claimed methods for detecting GapC antibodies, and to raise antibodies that are used in claimed methods for detecting GapC proteins
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100.0%; Pred. No. 8.6e-145;
ive 0; Mismatches 0;
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

C Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

C Streptococcus in a bacteria (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity or antigrial or attention or allocation or distinguishing/identifying
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Nucleic
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                                                                                                                    New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
Ö
 Grandi
 Margarit Y RosI,
                                                                                                                                                                                                        Claim 1; Page 4031; 4525pp; English
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  Masignani
                                                           WPI; 2002-352536/38
N-PSDB; ABN70591.
 Telford J,
Tettelin H;
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Sequence 336 AA;

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Length 336;
                     Indels
Score 1714; DB 5;
Pred. No. 1.1e-144;
1; Mismatches 0;
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llarity 99.7%;
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cell proliferation; drug
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            ABU46455 standard; protein; 336
                                                                            Protein encoded by Prokaryotic
                                                        (first entry)
                                                        19-JUN-2003
ABU4645
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design.

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The invention relates to an isolated nucleic acid comprising any one of the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a call. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operor required for proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation, (7) identifying a compound that inhibits proliferation of an ordinated pathway in which a proliferation required for cellular proliferation or the biological pathway required for proliferation or that that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent or collection of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational deruging processed; (12) determining the expert of compound, and proteins or for screening for homologous nucleic acids are useful for equired for proliferation to isolate candidate molecules for rational deruging proversy programs, or for screening for homologous nucleic acids are better the target prokarycit essential genes. Note: The sequence data for this patent did not format direct
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screfor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                        Ohlsen
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Pred. No. 1.1e-144;
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                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 74379; 1766pp; English.
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                                                                                                                                                                                                                                                                                                         Aalone C,
Carr GJ,
                                                                                                                                                                  2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
                                                                                                                                                     2001US-00815242
                                                                                                                2002WO-US009107
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                                                                                                                                                                                                                                                                                                          Malone
                                                                                                                                                                                                                                                                     (BLIT-) ELITRA PHARM INC.
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 Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                    2003-029926/02
B; ACA50325.
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                                      WO200277183-A2.
                                                                                                                                                                     06-SEP-2001;
25-OCT~2001;
08-FEB-2002;
06-MAR-2002;
                                                                                                                                                21-MAR-2001;
                                                                                                               21-MAR-2002;
                                                                          03-OCT-2002
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Best Local
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Wall
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be
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                                                                                                                                                      QRVPVPT
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                                                                                                      YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAA
                                                                                                                                                YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAA
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                                                                                                                                                                                                                                                                                                                   336
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                                                                                                                                                                                                                                                                                                                  EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP29106 standard; protein; 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000; 2000GB-00026333
24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
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INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pyogenes.
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Pettelin H;
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New DNA encoding bacterial plasmin receptor - useful as thrombolytic agents, used with plasminogen activator or bound to plasmin, also useful in vaccines against bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                               190 YTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT
                                                                                                                                                                                                                                                                                            TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA
                                                                                                                                                                                                              121 TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA
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                                                                                                                        Gaps
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used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins
                                                                                          Length 345;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lottenberg
                                                                                         Query Match
Best Local Similarity 99.9%; Score 1714; DB 5;
Best Local Similarity 99.7%; Pred. No. 1.1e-144;
Matches 335; Conservative 1; Mismatches 0;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes
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N-PSDB; AAQ70705.
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                                                              Sequence 345 AA;
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16-MAY-1990;
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22-FEB-1995
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AAR56486
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This sequence represents the S. pyogenes plasmin receptor. The DNA encoding this sequence was isolated from the S. pyogenes clinical isolate 64/14. The plasmin receptor has a very high affinity for plasmin which, when bound, retains its enzymatic activity but is not regulated (inhibited) by alpha-2-antiplasmin. The receptor protein, when administered concurrently or sequentially, prolongs the activity of plasminogen activator (PA) so allows a reduction in dose, and thus lowers the risk of bleeding, and may prevent reocclusion of blood vessels. The protein may be coupled to a fibrin-specific monoclonal antibody to provide targetting to clots. The plasmin receptor may be useful in human or veterinary medicine, for treatment of thrombosis and pulmonary embolism, and for solubilising clots in catheters or shunts. (Updated on 25-MAR-2003 to correct PF field.)
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Pred. No. 2e-144;
2; Mismatches
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90US-00524411.
92US-00928462.
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                                                                                                                                                                                                            Sequence 336 AA;
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16-MAY-1990;
10-AUG-1992;
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AAY85681
ID AAY85681
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                                                                                                                                                                                               Polynucleotide sequence AAC66140 encodes the Streptococcal plasmin receptor protein AAY85681. The protein is used in a method for raising immune response in a mammal. The method comprises administering the plasmin receptor protein. The method is useful as a vaccination against group A Streptococcal infections and potentially against a broad range cinfections associated with pathogens expressing glyceraldehyde-3-phosphate dehydrogenase (GAPDH) or GAPDH-like proteins at their cell surfaces. The vaccine has antibacterial and antihelminthic activity
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                                                                                       Raising an immune response in a mammal, especially for vaccination against group A streptococcal infections, comprises administering a solated streptococcal plasmin receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 336;
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     Boyle MDP
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                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 99.4%; Score 1711; DB 4; Similarity 99.4%; Pred. No. 2e-144; 4; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus GapC multiepitope fusion PolyGap4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50664 standard; protein; 448 AA.
                                                                                                                                                                  Claim 2; Col 27-30; 17pp; English
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Streptococcus agalactiae.
Streptococcus parauberis.
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(first entry)
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     Broder
                                   2001-006210/01.
B; AAC66140.
                                                                                                                                                                                                                                                                                                                                                                   Sequence 336 AA;
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  Von Mering G,
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08-APR-2002
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                                                      N-PSDB;
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The present sequence is that of a novel multiple epitope fusion protein, designated PolyGap4, comprising the entire amino acid sequence of the Streptococcus dysgalactiae GapC plasmin binding protein in addition to unique amino acid sequences from the Streptococcus parauberis and Streptococcus agalactiae GapC proteins. The multiple epitope protein is produced in host cells transformed with an expression vector comprising a chimaric gene (see ABA91327) encoding the protein. PolyGal4 is an example of novel GapC multiple epitope fusion proteins of the invention that comprise epitopes from 1 or more of S. dysgalactiae, S. agalactiae, S. parauberis, Streptococcus uberis and Streptococcus iniae (see AAM50665-69). The multiple epitope fusion proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcus infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope protein is capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448;
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Pred. No. 2.2e-139;
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                                                                                                                        Fontaine M;
                                                                                                                                                                                                                                                                                                     Claim 9; Fig 6A-C; 116pp; English.
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               11-JUN-2001; 2001WO-CA000836.
                                                     2000US-0211247P
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                                                                                                                        Perez-Casal J,
                                                                                        SASKATCHEWAN
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N-PSDB; ABA91327.
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335; Conser
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Best Local S
Matches 335
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The present sequence is that of the GapC plasmin binding protein,

UberGapC, of Streptococcus uberis ATCC 9927. The invention relates to

novel GapC multiple epitope fusion proteins that comprise epitopes from 1

or more of Streptococcus dysgalactiae, Streptococcus agalactiae,

Streptococcus parauberis, Streptococcus uberis and Streptococcus iniae

Streptococcus parauberis, Streptococcus uberis and Streptococcus iniae

(see AAM50665-69). A claimed example is PolyGap4 (see AAM50664).

Expression vectors and host cells for production of the multiple epitope proteins are used in fusion proteins are provided. The multiple epitope proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection in a mastitis. They are also used in claimed methods of detecting sre capable of Streptococcus antibodies. The multiple epitope proteins are capable of Streptococcus antibodies. The multiple epitope proteins are capable of streptococcus immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation while minimising the number of antigens present in the final formulation was an advantable of antigens present in the final formulation costs
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                                                                                                                                                                                                                                                  infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel GapC multiple epitope fusion polypeptide comprising antigenic determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, parauberis, or S. iniae GapC protein useful for treating mastitis in
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                                                                                                                                                                                                  Streptococcus uberis gapC plasmin binding protein UberGapC.
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92.9%; Pred. No. 4.1e-136;
ive 15; Mismatches 9;
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                                              AAM50667 standard; protein; 336 AA
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N-PSDB; ABA91330.
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                                                                                                                                                                                                                                                      GapC;
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                                                                                                                                                                                                                                                      UberGapC; Gap(
immunisation;
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                                                                                                                                                                                                                                                          LMTTIHA
                                                                                                                                                                                                                          LTQTKVM
TAPGGDDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALQDNFGVKQGI
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diagnosis; therapy.
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Pred. No. 4.1e-136;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                          TVDGNQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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ilarity 92.9%;
Conservative 15
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cattle, horse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-2001;
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a
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9
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                                                                                TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA
MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV
                                                                                                                                                         YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT
                            KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus protein for the treatment or prevention of disease caused by Streptococcus bacteria, such as meningitis, detecting a compound that binds to the protein.
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                                                                                                       standard; protein;
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INST GENOMIC RES.
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N-PSDB; ABN71389.
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                                                                                                                                                                                                            FDGTVEV
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biological sample. (I) is used to determine whether a compound (I). A composition comprising (I) or a nucleic acid encoding (I) used as a vaccine or diagnostic composition. The disease caused Streptococcus that is prevented or treated may be meningitis. Nacid encoding (I) may be used to recombinantly produce (I) and used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins
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                                                                                                                                                     Score 1609; DB 5;
Pred. No. 2.6e-135;
7; Mismatches 10;
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                                                                                                                                                     Query Match
Best Local Similarity 92.0%;
Matches 309; Conservative 1
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N-PSDB; ABA91329.
                                                                                                                           Sequence 336 AA;
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The present sequence is that of the GapC plasmin binding protein,
AgalGapC, of Streptococcus agalactiae ATCC 27541. The invention relates
to novel GapC multiple epitope fusion proteins that comprise epitopes
from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae,
Streptococcus parauberis, Streptococcus uberis and Streptococcus iniae
(see AAM50665-69). A claimed example is PolyGap4 (see AAM50664).

Expression vectors and host cells for production of the multiple epitope
(claimed vaccines for treating or preventing a bacterial infection in a
vertebrate, especially a streptococcal infection, and particularly
mastitis. They are also used in claimed methods of detecting
Streptococcus antibodies. The multiple epitope proteins are capable of
eliciting broad immunity against a variety of streptococcal infections
while minimising the number of antigens present in the final formulation
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                                                                                                                                                                                                                                                                                                                                                   93.4%; Score 1602; DB 5;
larity 91.7%; Pred. No. 1.1e-134;
Conservative 17; Mismatches 11;
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 2A-B; 116pp; English.
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Best Local Similarity
Matches 308; Conserva
                                                                                                                                                                                                                                                                                                                   Sequence 336 AA;
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Fig
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2000US-0211022P

-JUN-2000;

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The present sequence is that of the GapC plasmin binding protein

(AgalGapC) of Streptococcus agalactiae ATCC 27541, encoded by the GapC

gene given in ABA91249. GapC, which has no signal sequence or membrane

anchor domain, is capable of eliciting an immune response in a

vertebrate. The invention provides the GapC genes and proteins of 5

Streptococcus species, as well as recombinant vectors, host cells and

vaccine compositions comprising GapC polynucleotides or proteins. The

vaccines are used to treat or prevent a bacterial infection, especially a

streptococcal infection, and mastitis in particular (claimed). GapC

c vaccines are also used in claimed methods for detecting

streptococcal infection and mastitis in particular (claimed). GapC

c proteins are also used in claimed methods for detecting

and to raise antibodies that are used in claimed methods for detecting

GapC proteins. S. agalactiae is a common pathogen associated with

mastitis in cattle, horse, sheep and goat. It also causes septicemia,

meningitis, bacteraemia, impetigo, arthritis, urinary tract infections,

c abcesses, spontaneous abortion, etc
                                                                                                                               S.agalactiae,
                                                                                                                                                            brates.
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                                                                                                                          Novel isolated GapC protein of Streptococcus dysgalactiae, S.ag
S.uberis, S.parauberis, or S.iniae, useful as vaccine component
treating streptococcal infection which causes mastitis in verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 336;
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Pred. No. 1.1e-134;
7; Mismatches 11;
                                                 Potter
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                                              Σ
                                                 Fontaine
                                                                                                                                                                                            English
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91.7%;
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(first entry)
                 (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                               Perez-Casal
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N-PSDB; ABA91249.
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11-FEB-2003
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the experishication (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS5494. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleorides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the target sequence, and where the parts of the primers having the target sequence, and where the parts of the primers having complementary to compound with the protein, and determining whether the test compound with the protein, and determining whether the test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus promementary to the proteins.

The amplified, assumptions become rendered inactive. The proteins and antibiodise bacterium, where one or more genes bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, ottis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiodies. The methods are useful for identifying expensed by the identified coding regions from the genomic sequence. Note: The sequence data for this parent diagnostic form part of the printed or sequence data for this parent diagnostics and antibiodies. The present sequence is competed to the proteins of sequence data for this parent diagnostics and antibiodies. The present sequence is competed to the protein of sequence of the whole in the protein of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection.
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   respiratory;
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 auditory;
  immunostimulant;
                                                                 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4188; 56pp; English.
                                                                                                                                                                                                                                                                                                                                               Fraser
   antibacterial;
                                                                 4
                                                                Streptococcus pneumoniae, type
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                                                                                                                                                                                          2002WO-IB002163
                                                                                                                                                                                                                                                                                                                                            Tettelin H,
                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
                        vaccine
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nes 311; Conser
antiinflammatory;
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                                                                                                         WO200277021-A2.
                     gene therapy;
                                                                                                                                                                                          27-MAR-2002;
                                                                                                                                                                                                                                                                                                                                            Masignani V,
                                                                                                                                                 03-OCT-2002
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Matches
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic
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                                                                                                               QRVPTPT
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LMTTIHA
               TAPGGNDVKTVVFNTNHDVLDGTETVISGASCTTNCLAPMAKALQDNFGVVEGLMTTIHA
                                                       QRVPVPT
                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                        YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAA
TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKG
                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae cellular proliferation protein #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                 AAU37576 standard; protein; 359 AA
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2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
2000US-0253625P.
2000US-0257931P.
2001US-0269308P.
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                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELITRA PHARM INC
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N-PSDB; AASS5435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200170955-A2.
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                            14-FEB-2002
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cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                    GSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM
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                                                                                                 Query Match
Best Local Similarity 92.6%; Pred. No. 6.9e-134;
Matches 311; Conservative 12; Mismatches 12;
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Job time : 63 secs
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Title:

MVVKVGINGFGRIGRLAFRR.. US-10-650-369-12 1715 BLOSUM62 Gapop 10.0 score: Scoring table: Sequence: Perfect

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51625971 residues 389414 segs, Searched:

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. score gand is

SUMMARIES

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Result No.

Sequence 6, Appli Sequence 21612, A	equence 6, Appl	equence 186, Ap	equence 3783, A	equence 11, App	equence 9, Appl	equence 13, App	equence 11854,	equence 6704, A	equence 3378, A	equence 3470, A	e 6082, A	equence 19846,				
US-08-903-800A-6 US-09-252-991A-21612	-09-674-826B-6	7-080-18	7-362-18	-095-855-1	4-542-18	-09-205-426-18	-09-134-001C-3	-532-803-1	-532-80	S-09-548-938A-1	-489-039A-11	-328-352-670	-540-236-337	0-236-347	-543-681A-608	2-991A-19
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RESULT 1
US-09-878-766A-12
i Sequence 12, Application US/09878766A
i Patent No. 6660270
i GENERAL INFORMATION:
i APPLICANT: Porter, Andrew A.
APPLICANT: Porter, Andrew A.
APPLICANT: Portaine, Michael
ITILE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
ITILE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
ITILE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 336
TYPE: PRT
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Pred. No. 4.2e-164;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                         100.0%; Sc
100.0%; Pr
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
FILING DATE: 19920810
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
     Sequence 2, Application US/07928462
; Sequence 2, Application US/07928462
; Patent No. 5328996
; GENERAL INFORMATION:
; APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
; APPLICANT: Broder, Christopher C.
APPLICANT: Broder, Christopher C.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
; TITLE OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1711; DB 1;
Pred. No. 1.1e-163;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-13.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                         ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 99.4%;
Matches 334; Conservative
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ZIP: 32606
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ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,247
301 EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK 336
                                                                                                                                                                                 APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
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                    301 EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, 8
CITY: Gainesville
                                                                                                                           Sequence 2, Application US/08273247
Patent No. 6136323
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
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TYPE: amino acid
TOPOLOGY: linear
MECULE TYPE: protein
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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US-08-273-247-2
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US-09-878-766A-22

Sequence 22, Application US/09878766A

Patent No. 6660270

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Potter, Anchael

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

TITLE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 5.1e-158;
0; Mismatches 1;
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RESULT 5 US-09-878-766A-16

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; Sequence 16, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NOS: 22
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus uberis
US-09-878-766A-16
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APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 91.7%; Pred. No. 9.9e-153;
Matches 308; Conservative 17; Mismatches 11;
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Patent No. 6660270
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 336
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RESULT 7
US-09-878-766A-20
i Sequence 20, Application US/09878766A
j Patent No. 6660270
j GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
TITLE OF INVENTION AGAINST STREPTOCOCCUS INFECTION
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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nes 304; Conser
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JAPPLICANT: Potter, Andrew A.

JAPPLICANT: Fontaine, Michael

JAPPLICANT: APPLICATION NUMBER: US/09/878,766A

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT APPLICATION NUMBER: 2.0

JAPPLICATION NUMBER: 2.0

JAPPLICANT: APPLICATION NUMBER: US/09/878,766A

JAPPLICANT: APPLICANT: US/09/878,766A

CURRENT APPLICATION NUMBER: US/09/878,766A

JAPPLICANT: APPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

JAPPLICANT: US/09/878,766A

JAPPLICANT: US/09/878,766A

JAPPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

JAPPLICANT: US/09/878,766A

CURRENT APPLICANT: US/09/878,766A

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Streptococcus pneumoniae Antigens and Vaccines
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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Pred. No. 2.6e-150;
6; Mismatches 15;
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Sequence 54, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Streptococcus parauberis
US-09-878-766A-18
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Best Local Similarity 90.8%;
Matches 305; Conservative 1
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TITLE OF INVENTION: St.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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ZIP: 20850
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US-09-878-766A-18
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CITY: RO
STATE: M
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FILING DATE: 30-Oct-1997
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US-09-134-000C-4400
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                                                                                                                                                                                                                                                                                                                        Length 333;
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Patent No. 6573082

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                      Score 1549.5; DB 3;
Pred. No. 1.9e-147;
2; Mismatches 16;
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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  US/08/961,083
                                                                                                               36,373
R: PB340P2
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il Similarity 91.3%; Pi
303; Conservative 12;
                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                        54:
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                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    333 amino acids
                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein -08-961-083-54
                              SSIFICATION: 435
APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 43
                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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US-09-536~784-54
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Best Local (
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Sequence 4400, Application US/09134000C

Sequence 4400, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT FILING DATE: 1998-08-13

PRIOR PELLING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 4400

LENGTH: 346
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Best Local Similarity 91.3%; Pred. No. 1.9e-147;
Matches 303; Conservative 12; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-536-784-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Enterococcus faecalis
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Sequence 5513, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn boucette-Stamm et al
APPLICANT: Lynn boucette-Stamm et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE REFERENCE: GTC-007
TITLE OF INVENTION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5513
LENGTH: 348
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                                                                                                DB 4;
                                                                                              ch 1325.5; DB 4; Score 1325.5; DB 4; I Similarity 77.8%; Pred. No. 6.3e-125; 260; Conservative 25; Mismatches 48;
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 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...333
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US-09-107-532A-4769
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Best Local Similarity
Matches 234; Conser
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US-09-134-001C-5513
FEATURE
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US-09-107-532A-4769

; Sequence 4769, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; GENERAL INFORMATION:

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO

: TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO
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                                                 FDGTVEV
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                   Gaps
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                                                                    MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGR
                  Indels
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 Pred. No. 4.1e-125; ; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
'ORMATION FOR SEQ ID NO: 4769:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPE
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: July 2, 1 INFORMATION:
                   24;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
.4%;
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Similarity 78., 2; Conservative
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                262;
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    Local
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Matches
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RESULT 14
US-09-134-000C-4229
i Sequence 4229, Application US/09134000C
i Patent No. 6617156
i GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ITILE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
ITILE REFREENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4229
LENGTH: 357
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SIFDPTQ
             FDGTVE
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YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT
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; Sequence 233, Application US/0963423
; Patent No. 6544772
; GENERAL INFORMATION:
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Havukkala, Ilkka J.
Bloksberg, Leonard, Lubbers, Mark W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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197; Conser
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APPLICANT:
APPLICANT:
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APPLICANT: Christensson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynuclectides, materials inc
TITLE OF INVENTION: them and methods for using the
FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                    56.3%; Score 966; DB 4; ilarity 57.0%; Pred. No. 9.4e-89; Conservative 48; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: May 11, 2004, 16:50:40
                                                                                                                                                                                                       ; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-233
                                                                                                                                                                                                                                                                      Similarity
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LENGTH: 340
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 11, 2004, 16:45:46; Search time 21 Seconds (without alignments) 1539.064 Million cell updates/sec

US-10-650-369-12 1715 1 MVVKVGINGFGRIGRLAFRR.....EMSYTAQLVRTLEYFAKIAK 336 score: Title: Perfect so Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	scription	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde 3-	lyceraldehyde-3-	ypothetical prot	hypothetical prote	lyceraldehyde-3-	lyceraldehyde 3-	lyceraldehyde 3-	lyceraldehyde 3-	lyceraldehyde-3-	lyceraldehyde 3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde 3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde 3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-	robable glyceral	lyceraldehyde-3-	lyceraldehyde-3-	lyceraldehyde-3-
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ALIGNMENTS

ድ <i>ጳ</i> መጀ ⁸	RESULT 1 A42963 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococcus N;Alternate names: plasmin receptor
	inge 03-Jun-2002
K 17	R, Lottenberg, R.; Broder, C.C.; Boyle, M.D.; Kain, S.J.; Schroeder, B.L.; Curtiss III, I. Bacteriol. 174, 5204-5210, 1992
) K K	A; Title: Cloning, sequence analysis, and expression in Escherichia coli of a streptococo A; Reference number: A42963; MUID: 92355491; PMID: 1322883
K K A	A;Accession: A42963 A;Molecule type: DNA B:Pesidnes: 1-336 <1.OT>
. « «	A;Experimental source: group A, strain 64/14 A:Note: sequence extracted from NCBI backbone (NCBIP:110308)
	A, Accession: B42963
	R; Molecule Lype: procein R; Residues: 2-74;161-164,'X',166-174;187-211,'X',213-217 <lo2> B: Bancholi V : Fischetti V A</lo2>
	A,Title: A major surtace protein on group A streptococci is a glyceraldenyde-s-phosphate A;Reference number: JH0750; MUID:92364544; PMID:1500854
A A	A; Accession: JH0750
	A,Roiccure 17Fc. procein A,Residues: 2-30,'A',32-40 <pan> C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase</pan>
O (24	C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase F;152/Active site: Cys #status predicted
	Query Match Best Local Similarity 99.4%; Pred. No. 4.2e-116; Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
о —	Oy 1 MVVKVGINGFGRIGRLAFRRIONVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV 60
Ω	DD 1 MVVKVGINGFGRIGRLAFRRIQNIEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV 60
o 	Qy 61 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI 120
Δ	DD 61 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI 120
Ο	Qy 121 TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA 180
Ω	Db 121 TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA 180
<i>o</i>	Oy 181 YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT 240
Ω	Db 181 YTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAORVPY 240
····	Qy 241 GSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM 300

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Gyeraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [imported] - St Cypecies: Streptococcus pneumoniae
Cybecies: Streptococcus pneumoniae
Cybecies: Streptococcus pneumoniae
Cybecies: Streptococcus pneumoniae
Cybecies: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
CyAccession: 098099
Rydoskins, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N.
Cy, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Residues: 1-359 «KUR>
A;Residues: 1-359 «KUR>
A;Residues: 1-359 «KUR>
A;Gene: gapA
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: oxidoreductase
                                                           GSPDB:GN00164;
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llarity 92.6%; Pred. No. 1.4e-107;
Conservative 12; Mismatches 12;
                                                           PIDN: AAK76079.1;
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-335 <KUR>
A;Cross-references: GB:AE005672; PIDN
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2012
C;Superfamily: glyceraldehyde-3-phospl
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glyceraldehyde 3-phosphate dehydrogenase [imported] - Streptococcus pneumoniae (strain I C; Species: Streptococcus pneumoniae
C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C; Accession: F95235
R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Reference number: A95000; MUID:21357209; PMID:11463916
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glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1... Glycession: Streptococcus "equisimilis"
C; Species: Streptococcus "equisimilis"
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 0. C; Accession: S71350
R; Gase, K.; Gase, A.; Schirmer, H.; Malke, H.
Eur. J. Biochem. 239, 42-51, 1996
A; Title: Cloning, sequencing and functional overexpression of the inding protein. Purification and biochemical characterization of A; Reference number: S71350; MUID:96305364; PMID:8706717
A; Accession: S71350
A; Residues: 1-336 GAS>
A; Cross-references: EMBL:X97788; NID:g1478268; PIDN:CAA66377.1; PA; Experimental source: strain H46A
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C; Keywords: gluconeogenesis; glycolysis; NAD; oxidoreductase
C; Keywords: gluconeogenesis; glycolysis; NAD; oxidoreductase
F; 4-34/Region: beta-alpha-beta NAD nucleotide-binding fold
F; 152/Active site: Cys #status predicted
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                                                                                                                        GSPDB:GN0014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - C (Species: Clostridium pasteurianum C;Species: Clostridium pasteurianum C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-Jun-2002 C;Accession: S34254
R;Oster, T.; Assobhei, O.; Scherrer, S.; Branlant, G.; Branlant, C. submitted to the EMBL Data Library, May 1993
A;Description: Nucleotide sequence of the glyceraldehyde-3-phosphate dehydro A;Reference number: S34254
A;Accession: S34254
A;Molecule type: DNA
A;Residues: 1-334 < OST>
A;Cross-references: EMBL:X72219; NID:g311923; PIDN:CAA51020.1; PID:g311924 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM
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                     acid bacterium 37471
Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacteriu A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Accession: G86694
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-337 <STO>
A; Residues: 1-337 <STO>
A; Residues: 1-337 <STO>
A; Coss-references: GB:AE005176; PID:g12723446; PIDN:AAK04657.1;
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: gapA
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EV-DGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK 336
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                                                                                                                                                                                                                      Score 1338.5; DB 2;
Pred. No. 3.2e-89;
1; Mismatches 45;
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llarity 74.3%;
Conservative 33
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ilarity 77.2%;
Conservative 3
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Best Local Similarity
Matches 249; Conser
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Best Local
Matches 26
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S34254
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F86905
hypothetical protein gapB [imported] - Lactococcus lactis subsp. lactis (strain ILL).
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: F86905
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Genome Res. 11, 731-733, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lact A;Reference number: A86625; MVID:21235186; PMID:11337471
A;Residues: preliminary
A;Accession: F86905
A;Accession: F86905
A;Accession: F86905
A;Residues: 1-336 - SIO>
A;Residues: 1-336 - SIO>
A;Coss-references: GB:AE005176; PID:g12725315; PIDN:AAK06344.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: gapB
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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G86694
hypothetical protein gapA [imported] - Lactococcus lactis subsp. lactis (st:
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: G86694
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenba
                                                                                                                                   GSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM
                                                                MTTIHA
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                                                                                                                                                      GSVTELVVTLDKAVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM
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TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIOKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.2%; Score 1410; DB 2;
larity 81.2%; Pred. No. 2.2e-94;
Conservative 22; Mismatches 41
                                                                                                                                                                                                     EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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Best Local S
Matches 273
                                   144
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121
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DD 120 APAGNDLKTIVFNVNNEDLDGTETVISGASCTTNCLAPMAKVLNDKFGIEKGFMTTIHAY 179	ession: AD1751
182 TGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPTG 24	Jaser, F.; Frangeu Dominguez-Bernal, Jones, L.M.; Kars
180 TNDONTEDGPHRKGDFRRARAAVSIIPNSTGAAKAIAQVIPELKGKUDGNAQRVPVFTG 23	ience 294, 849-852, 2001 Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenc
OY 242 SVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVME 301 : :	, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Fitle: Comparative genomics of Listeria species. Reference number: AB1077; MUID:21537279; PMID:11679669
Qy 302 VDGSQLVXVVSWYDNEMSYTAQLVRTLEYFAKIAK 336	ccession: AD1751 tatus: preliminary olecule type: DNA
OO VDGSQLVAIVSWIDNEMSIISQLVKILBIFAKIAK 3	Kesidues: 1-3. Cross-referen Experimental
	Sene: gap
yde s-phosphare denydrogenase homorog gap (imported) - bisteria Listeria monocytogenes	superramily: glyceraldenyde-3-phosphate denydrogenase
Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 : AC1382	Match ocal Similarity 73.3%; Pred. No. 1.3e-83;
.; Frangeul z-Bernal, G	Matches 247; Conservative 32; Mismatches 56; Indels 2; Gaps
4.; Karst, U. 349-852, 2001	1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV
<pre>Kreft, J.; Kuhn, M.; Kunst, F.; Kur lueter, T.; Simoes, N.; Tierrez, A.</pre>	1 MTVKVGINGFGRIGRLAFRRIQNVEGIEVVAINDLTDAKMLAHLLKYDTTQGRFDGEVEV
<pre>mparative genomics of Listeria species. number: AB1077; MUID:21537279; PMID:11679669</pre>	61 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI
. AC138 relimin	kvlanrnpeelpwgdlgvdivlectgfftaqdkaelhika-gakkvvi
type: DNA 1-336 <gla< td=""><td>GGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA</td></gla<>	GGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA
erences:	TĹĎĠŤĔŤVÍSGAŚCŤŢŃĊĽĀPMAKVĽEDKFGVVEGLMTTIHA
	Qy 181 YTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT 240
C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase	DD 180 YTGDQNTLDAPHPKGDFRRARAABNIIPNTTGAAKAIGEVLPTLKGKLDGAAQRVPVPT 239
Query Match Best Local Similarity 73.3%; Pred. No. 1.1e-83; Matches 247; Conservative 33; Mismatches 55; Indels 2; Gaps 2;	Qy 241 GSVTELVVTLDKNVSVDEINAAMKAASN-DSFGYTEDPIVSSDIVGVSYGSLFDATQTKV 299 : :::
1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV	300 MEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK :
I MIVKVGINGFGRIGRLAFRRIQNVEGIEVVAINDLTDAKMLAHDLKYDTTQGRFDGEVEV 6	DD 300 DIVGDQQLVKIVAWIDN&MSIIAQLVKILBIFAKIAN 330
Qy 61 KEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI 120	SULT 10 6987
Oy 121 TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA 180	raidenyde 3-phosphate denydrogenase, gene gapo limported) - crostridium accobacy. cies: Clostridium acetobutylicum e: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
181 YTGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT 24	Nolling, J.; Breton, G.; Daly, M.J.; Bennett, G.
DD 180 YTGDQNTLDAPHPKGDFRRARAAENIIPNTTGAAKAIGEVLPTLKGKLDGAAQRVPVPT 239	Bacteriol. 183, 4823-4838, Title: Genome Sequence and Peference number: 196900. M
241 GSVTELVVTLDKNVSVDEINAAMKAASN-DSFGYTEDPIVSSDIVGVSYGSLFDATQTKV 29	Accession: C96987 Status: preliminary
240 GSLTELVTVLDKKVTVDEVNAAMEAASDPETFGYTSDQVVSSDIKGMTFGSL	Molecule type: DNA Residues: 1-334 <kur></kur>
Oy 300 MEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK 336 :	Cross-references Experimental sou Genetics:
	Gene: Super
AD1751 AD1751 glyceraldehyde 3-phosphate dehydrogenase homolog gap [imported] - Listeria innocua (stra C; Species: Listeria innocua C; Species: 27-Nov-2001 #sequence revision 27-Nov-2001 #text change 14-Dec-2001	Query Match Best Local Similarity 71.9%; Pred. No. 1.6e-83; Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

RESULT 12 Ballon 300 TVGGKQLVKTVAMYDNEMSYTCQLVRTLEYFA 331 RESULT 12 Ballon 4 Bellon 5-phosphate dehydrogenase NWB2159 [imported] - Neisseria meningitidis (st c) Species: Neisseria meningitidis R) Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; K.; H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A,Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A,Reference number: A81000; MUID:2017575; PMID:10710307 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-334 <-TET> A,Experimental source: Serogroup B, Strain MC58 C,Genetics: A,Genetics: A,Gen	tch al Similarity 69.3%; 230; Conservative 3 1 MVVKVGINGFGRIGRLAFR	RESULT 13 E89850 glyceraldehyde-3-phosphate dehydrogenase [imported] - Staphylococcus aureus (strain N315 clyspecies: Staphylococcus aureus cypecies: Staphylococcus aureus cypecies: Staphylococcus aureus cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 cypecies: Nota, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Status: Dreliminary A; Molecule type: DNA A; Status: Dreliminary A; Molecule type: DNA A; Residues: 1-336 < KUR> A; Residues: 1-336 < KUR> A; Experimental source: strain N315
2 VVKVGINGFGRIGRIAFRRIQNVEGVEVTRINDLIDPNMLAHLLKYDTTQGRFDGTVEVK 61 3	RESULT 11 B82019 B82019 G192craldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) C NWA0246 (impo c) Species: Neisseria meningitidis C; Accession: B82019 Nature 404. 502-506, 2000 A; Farkhill, J.; Achtuan, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Monel Nature 404. 502-506, 2000 A; Farkerence number: A81775; MUDI:2022556; PMID:10761919 A; Accession: B82019 A; Accession: B820	KEGGFEUNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVI 120

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completed: May 11, 2004, 16:49:49
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R; Branny, P.; Delatorre, F.; Garel, J.R.
Microbiology 144, 905-914, 1998
A; Title: An operon coding for three glycolytic enzymes in Lactobacillus delbrueckii
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A;Accession: T09633
A;Accession: T09633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-338 <BRA>
A;Residues: 1-338 <BRA>
A;Cross-references: EMBL:AJ000339; NID:g2624189; PIDN:CAA04014.1;
A;Experimental source: subsp. bulgaricus, strain B107
C;Genetics:
A;Gene: gap
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C;Keywords: gluconeogenesis; glycolysis; oxidoreductase
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Superfamily: glyceraldehyde-3-phosphate dehydrogenase
Keywords: gluconeogenesis; glycolysis; oxidoreductase
C;Genetics:
A;Gene: gap
C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
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                                                                     Score 1183; DB 2;
Pred. No. 5.3e-78;
3; Mismatches 62;
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68.2%;
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G'Species: Escherichia coli
C'Species: 18-Jul-2001
R'Accession: F90881
R'Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
Gaaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gencal A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
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59.3%; Pred. No. 2.7e-64;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 11, 2004, 16:42:06; Search time 18 Seconds (without alignments) 971.976 Million cell updates/sec Run on:

US-10-650-369-12 1715 1 MVVKVGINGFGRIGRLAFRR.....EMSYTAQLVRTLEYFAKIAK 336 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Y P5046	P3 Q8k8m	EQ Q59906 stre	P52987 lactococ	Q59309 clostrid	O52631 clostr	Q8cpy5 staphy	taphylo	O32755 lactobaci	P58072 escherich	P33898 escheri	P75358 mycopla	Q01651 coryneb	P47543 mycopla	J P09124 bacillus	P23722 bacillu	P00362 bacillu	P17721 thermotog	P46795 borrelia	067161 agr	Q92518 strept	ALTY P24165 sal	006822	P46713 mycobact	06977 escheric	P44304	P94915 mycob	RA Q9c136	YBB P1009	PO P78958 schizos	P5269	ヒタヒコ
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 335;
                                                                                                                                                                                                                                                                                                                                                                                             GLYCERALDEHYDE 3-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                      GROUP DURING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH. PATHWAY: Second phase of glycolysis; first step. SUBUNIT: Homotetramer (By similarity). SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the glyceraldehyde 3-phosp
                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Complete proteome.
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-> S (IN REF. 1).
F06006EE253CBA3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1709; DB 1;
Pred. No. 3.4e-111
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ACTIVATES THIOL G
(BY SIMILARITY).
A -> S (IN REF. 1
                                                                 glyceraldehyde
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(Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
de 3-phosphate dehydrogenase (EC
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Tam; PF02800; gpdh, C; 1.
Tam; PF02800; gpdh C; 1.
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35811 MW;
                                                                                                                                                                                              EMBL; M95569; AAA26953.1; -.
EMBL; AE006494; AAK33348.1; -
EMBL; AE009973; AAL97041.1; -
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ilarity 99.7%;
Conservative
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InterPro; IPR000173; GAP dhd
InterPro; IPR006424; GAPDH-I
                                                  SUBCELLULAR LOCATION: C
SIMILARITY: Belongs to
dehydrogenase family.
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335 AA;
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Q8K8M9;
28-FEB-2003 (Re]
28-FEB-2003 (Re]
15-MAR-2004 (Re]
Glyceraldehyde
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Glycolysis;
INIT_MET
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ID G3P_S
AC Q8KBN
DT 28-FE
DT 28-FE
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BY SIMILARITY.

GLYCERALDEHYDE 3-PHOSPHATE (BY
SIMILARITY).

ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MGAS315 / Serotype M3;
MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reveals
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Genome Res. 13:1042-1055(2003).

-!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN (By similarity).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

dehydrogenase family.
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strains and r
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                                                                                    Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M. Okahashi N., Kawabata S., Yamazaki K., Shiba T., Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus large-scale genomic rearrangement in invasive str
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Pred. No. 6.3e-111;
1; Mismatches 1;
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EMBL; AP005141; BAC63302.1; -.
InterPro; IPR000173; GAP_dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Complet INIT_MET 0 0 BY SIMILAR
(Plasminogen-binding protein) (Plasmin GAP OR FLR OR SPYM3_0201 OR SPS0207. Streptococcus pyogenes (serotype M3). Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                              TaxID=198466;
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                                                                                                                                                  SVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDAT
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EGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHTNGA
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Gase K., Gase A., Schirmer H., Malke H.;

"Cloning, sequencing and functional overexpression of the streptococcus equisimilis H46A gapC gene encoding a glyceraldehyde-3-phosphate dehydrogenase that also functions as glyceraldehyde-3-phosphate dehydrogenase that also functions as plasmin(ogen)-binding protein. Purification and biochemical characterization of the protein.";

Eur. J. Biochem. 239:42-51(1996).

-!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN.

-!- FUNCTION: D-glyceraldehyde 3-phosphate + phosphate NADH.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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o functions
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=119602;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2
(Plasminogen-binding protein) (Plasmin receptor)
GAP OR GAPC.
                                                                                                                                                                                                                 VDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X97788; CAA66377.1; -.
EMBL; Y12602; CAA73174.1; -.
PIR; S71350; S71350.
HSSP; P00362; 1GD1.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
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lycolysis; Oxidoreductase; NAD.
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Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I;
PROSITE; PS00071; GAPDH; 1.
                                                                                                                                                                                                                                                                                                                             STANDARD;
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STRAIN=H46A;
MEDLINE=96305364;
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PROSITE; Pa
Glycolysis
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61
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SEQUENCE FROM N.A.

STRAIN=IL1403;

MEDLINE=21235186; PubMed=11337471;

Meissenbach J., Wincker P., Mauger S., Jaillon O., Malarme K.,

Weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium Lactococcus

I lactis ssp. lactis IL1403.";

Genome Res. 11:731-753(2001).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

C -!- PATHWAY: Second phase of glycolysis; first step.

C -!- SUBUNIT: Homotetramer (By similarity).

C -!- SUBCELLULAR LOCATION: Cytoplasmic.

C -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

C -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
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                                                                                                                                                        VVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEVK
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                                                                                                                                                                                                                                                                     APGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHAY
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LM0230;
MEDLINE=95291425; PubMed=7773380;
Cancilla M.R., Hillier A.J., Davidson B.E.;
"Lactococcus lactis glyceraldehyde-3-phosphate dehydrogenase gene,
gap: further evidence for strongly biased codon usage in glycolytic
                          SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS (BY SIMILARITY).
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                                                                                               Length
              3-PHOSPHATE
                                                               FETACEDFD7663E46 CRC64;
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                                                                                                 Score 1612; DB 1;
Pred. No. 1.7e-104;
; Mismatches 13;
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01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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BY SIMILARITY.
GLYCERALDEHYDE
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pathway genes.";
Microbiology 141:1027-1036(1995)
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7
                                                                      35739 MW;
                                                                                                  94.0%;
95.5%;
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GAP OR LL0559.
                                                                                                                             Conservative
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151
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151
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Best Local S
Matches 320
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BINDING
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                                             ACT_SITE
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TMTTVHS
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                                                                                                                                                                                                   EMBL; L36907; AAC41453.1; -.
EMBL; L36907; AAC41453.1; -.
EMBL; AE006290; AAK04657.1; -.
PIR; G86694; G86694.
HSSP; P17721; 1HDG.
InterPro; IPR000173; GAPDH-I.
InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
T -> S (IN REF. 1).
T 17BB8C6AAEFF589D CRC64;
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Pred. No. 1.4e-85;
1; Mismatches 45;
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33P CLOPA

ID G3P CLOPA

AC Q59309;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2)

DE 17/CP 18).
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Bacteria; Firmicutes; Clostridia;
Clostridium.
NCBI_TaxID=1501;
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36057 MW;
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ilarity 77.2%;
Conservative 3:
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337 AA;
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RESP; P00362; IGD1.

RESP; P00044; GAPDH-I.

RESP; P00044; GAPDH-I.

RESP; P00078; GAPDH-I.

RESP; P00078; GAPDH-I.

RESP; P00078; GAPDH-I.

RESP; P00071; P00071; GAPDH-I.

RESP; P00071; P0007
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                                                                                                                                                           Flengsrud R., Skjeldal L.;
"Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806(1998).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
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T
G., Branlant databases.
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; Pred. No. 3.4e-82;
33; Mismatches 52;
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Oster T., Assobhei O., Scherrer S., Branlant G
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 VDGSQLVKTVSWYDNEMSYTSQLVRTLEYFAKIAK
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                                                                                                                                         PubMed=9629918;
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Best Local Similarity 74,3
Matches 249; Conservative
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                                                                                                            STRAIN=W5;
MEDLINE=98291870;
                                                                                     SEQUENCE
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collaboration
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                                                                                                                                                                                                                                                                                                                                           other
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSIS
                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GAP OR GAPC OR CAC0709.
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATAL
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                                                                                                                                                                                          [1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=99392446; PubMed=10463150;
Schreiber W., Durre P.;
"The glyceraldehyde-3-phosphate dehydrogenase of Clostridium acetobutylicum: isolation and purification of the enzyme, and sequencing and localization of the gap gene within a cluster of glycolytic genes.";
Microbiology 145:1839-1847(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF043386; AAC13160.1; -.

EMBL; AE007586; AAK78686.1; -.

PIR; C96987; C96987.

HSSP; P17721; 1HDG.

InterPro; IPR000173; GAP_dhdrogenase.

InterPro; IPR006424; GAP_DH-I.

Pfam; PF00044; gpdh; 1.

Pfam; PF02800; gpdh C; 1.

Pfam; PF02800; gpdh L; 1.

PROSITE; PR00078; G3P_DHDRGNASE.

TIGRFAMS; TIGR01534; GAPDH-I; 1.

PROSITE; PS00071; GAPDH-I; 1.

Glycolysis; Oxidoreductase; NAD; Complete protecome.

BINDING 150 GLYCERALDEHYDE 3-PHOSPHATE.

ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CAT.

SEQUENCE 334 AA; 35850 MW; 10C52A174BF789B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phonomy NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
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241; Conser
                                                                                                                                                                            TaxID=1488;
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Best Local S
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         APGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHAY
              TGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPYTG
                                                                           SVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVME
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151 151 GLYCERALDEHYDE 3-PHOSPHATE (BY
SIMILARITY).
178 ACTIVATES THIOL GROUP DURING CATALYSIS
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                       1.2.1.12) (GAPDH 1)
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                                                                                                                                                                                                                                                                                              G3P1 STAEP STANDARD; PRI; 336 AA. Q8CPY5; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.GAPA OR GAP OR SE0557. Staphylococcus epidermidis. Staphylococcus epidermidis. Bacteria; Firmicutes; Bacillales; Staphylococcus.
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                                                                                                                                                                                    VDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
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Pred. No. 4e-80;
D; Mismatches
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SEQUENCE FROM N.A.

STRAIN=Mu50 / ATCC 700699, and N315;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

A Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus

ureus.";

Lancet 357:1225-1240(2001).
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              ä
                                                          SAPAKGDVKTIVFNTNHDTLDGSETVVSGASCTTNSLAPVAKVLSDEFGLVEG
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., Cui L.,
                                         MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDT
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STRAIN=BB;
Morrissey J.A., Williams P.;
"Isolation and characterisation of a glycolytic operon in Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
61yceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12)
6APA OR GAP OR SAV0772 OR SA0727 OR MW0734.
Staphylococcus aureus (strain Mus) / ATCC 700699),
Staphylococcus aureus (strain MW2), and
Staphylococcus aureus (strain MW2), and
Staphylococcus aureus.
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MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulenc
                                                                                                                                                                                                                                                                                                                            MEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK 336
                                                                                                                                                                                                                                                                                                                                                           336
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 Pred. No. 2.6e-75; 
; Mismatches 62
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158879, 196620,
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 larity 69. Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                          similarity).
Nyde 3-phosphate
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GLYCERALDEHYDE 3-PHOSPHATE
SIMILARITY).
ACTIVATES THIOL GROUP DURIN
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate NADK.)

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADK.

PATHWAY: Second phase of glycolysis; first step.

SUBUNIT: Homotetramer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity)

SIMILARITY: Belongs to the glyceraldehyde 3-phosp dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1183; DB 1;
Pred. No. 7.9e-75;
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Mismatches
                                                                                                                                                                                                                                                EMBL; AJ133520; CAB38645.1; -...
EMBL; AP003360; BAB56934.1; -...
EMBL; AP003131; BAB41960.1; -...
EMBL; AP004824; BAB94599.1; -...
PIR; E89850; E89850.
SWISS-2DPAGE; Q925C5; STAAN.
HSSP; P17721; 1HDG.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF02800; gpdh, 1...
Pfam; PF02800; gpdh, 1...
PROSITE; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
Glycolysis; Oxidoreductase; NAD; Comple BINDING 151 151 GLYCERALDE
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68.2%;
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230; Conservative
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                                       (GAPDH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiology 144:905-914(1998).

**Aicrobiology 144:905-914(1998).

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phonomone + pho
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ACTIVATES THIOL GROUP DURING
(BY SIMILARITY).
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                                                              Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=1585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
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     update)
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Pred. No. 2.2e
5; Mismatches
                                  dehydrogenase
       annotation
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PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-1; 1.
PROSITE; PS00071; GAPDH; FALSE NEG.
Glycolysis; NAD; Oxidoreductase.
BINDING 156 156
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HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP_dhdr.
InterPro; IPR006424; GAPDH-I.
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ilarity 58.7%;
Conservative 45
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 28-FEB-2003 (Rel. 41, Last Glyceraldehyde 3-phosphate GAP.
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Pfam; PF02800; gpdh
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.I Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.
                                                                                                         GGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAK
                                                                                                                                                                                           PGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMT
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STRAIN=River isolate, and Clinical isolate;
MEDLINE=98283700; PubMed=9622357;
Espinosa-Urgel M., Kolter R.;
"Espinosa-Urgel M., Rolter R.;
"Escherichia coli genes expressed preferentially in an aquatic environment.";
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Hidalgo E., Limon A., Aguilar J.;
"A second Escherichia coli gene with similarity to gapA.";
Microbiologia 12:99-106(1996).
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ACTIVATES THIOL GROUP DUR (BY SIMILARITY).
A2F77CB2E773E64C CRC64;
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Enterobacteriaceae; Escherichia.
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ed. No. 1.1e-61;
Mismatches 76
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase C (EGAPC OR B1416/B1417.
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Pred.
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larity 59.3%;
Conservative 5
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Shao Y.;
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EMBL; L09067; AAA23856.1; ALT FRAME.
EMBL; AE000239; AAC74498.1; ALT FRAME.
EMBL; AE000239; AAC74499.1; ALT FRAME.
EMBL; D90780; BAA15033.1; ALT FRAME.
EMBL; D90781; BAA15038.1; ALT FRAME.
EMBL; M64541; -; NOT ANNOTATED CDS.
EMBL; X54798; CAA38569.1; -.
EMBL; X54798; CAA38569.1; -.
EMBL; M14166; AAA41178.1; -.
ECGGENE; EG12103; GapC.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.

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MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=3780374;

MEDLINE=87053179; PubMed=1 phosphate

I ibraries: evidence for a rat glyceraldehyde-3-phosphate

The construction of cDNA

Gehydrogenase-like mRNA and a ferritin mRNA within testis.";

DNA 5:427-435(1986).

L CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +

NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.

C -! - PATHWAY: Second phase of glycolysis; first step.

C -! - SUBUNIT: Homotetramer (By similarity).

C -! - SUBCELLULAR LOCATION: Cytoplasmic (Potential).

C -! - SUBCELLULAR LOCATION: Cytoplasmic (Potential).

C -! - SIMILARITY: Belongs to the glyceraldehyde 3-phosphate

dehydrogenase family.

C -! - CAUTION: IN THE K12 STRAIN THIS GENE IS DISRUPTED BY A STOP CODON

AND A FRAMESHIFT. IT SEEMS TO BE INTACT IN A NUMBER OF WILD
MEDLINE=97251357; PubMed=9097039; Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."; DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                           SEQUENCE OF 306-332 FROM N.A.
STRAIN=K12;
MEDLINE=92011371; PubMed=1917845;
Hidalgo E., Chen Y.-M., Lin E.C.C., Aguilar J.;
Molecular cloning and DNA sequencing of the Escherichia coli K-12 ald gene encoding aldehyde dehydrogenase.";
J. Bacteriol. 173:6118-6123(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: Ref.7 and Ref.8 sequences were originally thought to originate from rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=88232416; PubMed=2836696;
Nakamura H., Murakami H., Yamato I., Anraku Y.;
Nucleotide sequence of the cybB gene encoding cytochrome b561
"Nucleotide soli K12.";
Escherichia coli K12.";
Mol. Gen. Genet. 212:1-5(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krawetz S.A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases
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                                               NAD; Multigene family; Complete prote GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYS (BY SIMILARITY).
K -> Y (IN REF. 7 AND 8).
K -> Y (IN REF. 7 AND 8).
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European Bioinformatics Institute. There are no restricti
                                                                                                                                                                                              KVGINGFGRIGRLAFRRIQNVE-GVEVTRINDLTDPNMLAHLLKYDTTQGRFDG
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Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                               Length 333
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Nucleic Acids Res. 24:4420-4449(1996).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the glyceraldehyde 3-phosp
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1.2e-61;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC
GAPA OR GAP OR MPN430 OR MP411.
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TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD;
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        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eikmanns B.J.;
"Identification, sequence analysis, and expression of a
Corynebacterium glutamicum gene cluster encoding the three glycolytic
enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate
kinase, and triosephosphate isomerase.";
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GLYCERALDEHYDE 3-PHOSPHATE
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ACTIVATES THIOL GROUP DURING CATALYSIS
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                                                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                                                                                                                                                                                   , DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AA
                                                                                                                                                                                                                                                                                                                               ed. No. 1e-5
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 VDGNKLYKVYAWYDNESSYVNOLVRVVNYCAKL
                                                                                                                                                                                                                                                                                                                  Score 921;
Pred. No. 1
                                                                                                                     dhdrogenase
                                                                                    PIR; S73737; S.J. HDG.
HSSP; P17721; 1HDG.
InterPro; IPR000173; GAP_dhdrogenas(InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Alveolysis; Oxidoreductase; NAD; Cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 13059 / AS019;
MEDLINE=93015645; PubMed=1400158;
                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                         36805 MW;
                                                                                                                                                                                                                                                                                                                53.7%;
nilarity 54.1%;
Conservative 54
                                                                         AAB96059.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glyceraldehyde 3-phosphate
GAP OR CGL1588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                         337 AA;
                                                                                                                                                                                                                                                                                                                                 l Similarity
180; Conser
                                                                                                                                                                                                                                                              184
                                                                           AE000040;
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                                                                                                                                                                                                                                                              ACT SITE
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                            EMBL;
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Matches
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                                                                                                                                collaboration
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HGSIFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1SAPASNEDATFVYGVNHESYDPENHNVISGASCTINCLAPMAKVLNDKFGIENGLMTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYTGDOMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGSLFDA
                                                                                                                                                                                                                                                                                                                                                                                                      MVVKVGINGFGRIGRLAFRRI-QNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                         VKEGGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVV
                                                                                                                                                                                                                                                                                                                                                                                                                CGLMTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAKKVI
                                                                                                                                                                                                                                                                                                      Oxidoreductase, NAD; Complete proteome.

153 153 GLYCERALDEHYDE 3-PHOSPHATE.
180 180 ACTIVATES THIOL GROUP DURING CATALYSIS.
25 26 SD -> NG (IN REF. 1).
333 334 KL -> QALN (IN REF. 1).
334 AA; 36045 MW; 33792AF65FA90FA7 CRC64;
                                           3032
                                                             Ø
                                                             + phosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITAPGGNDVKTVVFNTNHDILD-GTETVISGASCTTNCLAPMAKALHDAFGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDDDSITVGGKRIAVYAERDPKNLDWAAHNVDIVIESTGFFTDANAAKAHIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YTEDPIVSSDIVGVS
                                         334;
                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                    Score 908.5; DB 1;
Pred. No. 7.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOTKVMEVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SGNTVKVVSWYDNEWGYTCQLLRLTELVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTGSVTELVVTLDKNVSVDEINAAMKAASNDSFG-
                           10025;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                   EMBL; X59403; CAA42045.1; -.
EMBL; AP005279; BAB98981.1; -.
PIR; A43260; A43260.
HSSP; P00362; 1GD1.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
Pfam; PF02800; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
                           / NCIB
 Bacteriol. 174:6076-6086(1992)
                                                                                                                                                                                                                                                                                                                                                                                     41;
                           / DSM 20300
                                                                                                                                                                                                                                                                                                                                                                     53.0%;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                    SEQUENCE FROM N.A.
STRAIN=ATCC 13032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLTKV
                                     Nakagawa S.;
                                                                                                                                                                                                                                                                                                       Glycolysis;
BINDING
                                                                                                                                                                                                                                                                                                                                                                                     190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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STRAIN=ATCC 33530 / G-37;

MEDLINE=96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Frieischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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GLYCERALDEHYDE 3-PHOSPHATE
(BY SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
4
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GAPA OR GAP OR MG301.
Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-81 AND 279-337 FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 337;

sequencing.";
J. Bacteriol. 175:7918-7930(1993).
J. Bacteriol. 175:7918-7930(1993).
CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phonomorphic and phase of glycolysis; first step.
PATHWAY: Second phase of glycolysis; first step.
SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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FAIEA1966687006B CRC64;
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InterPro; IPR006424; GAPDH-I.
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Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMB; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; CBINDING 157 157 GLYCE
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EMBL; U02213; AAD12507.1; -.
EMBL; U02178; AAD12463.1; -.
PIR; C64233; C64233.
HSSP; P17721; 1HDG.
TIGR; MG301; -.
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ilarity 53.2%;
Conservative 54
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177; Conser
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Best Local
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337

STANDARD;

G3P MYCGE

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122
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Furschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Euguano V., Carter N.M.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Fritz C., Fujita M., Fubret C., Ferrari E., Foulgar D.,
Fritz C., Fujita M., Fubret C., Ferrari E., Foulgar D.,
Fritz C., Fujita M., Fujita Y., Fume S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Achis B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mirzuno M., Moestl D., Nakai S., Noback M.,
Achis B., Rarooni E., Roponort G., Rey M., Reynolds S.,
Barro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Actesecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Sandie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Satouchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Ackiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
Ackiguchi M., Tamakoshi A., Tarkaji T., Tarkahashi H., Takemaru K.,
Ackier A., Wambutt R., Wedler E., Wedler H., Wannier F., Vasaumoto K., Yata K.,
Wiari A., Wambutt R., Yamamoto H., Yamane K., Yasaumoto K., Yata K.,
GGFEVNGNFIKVSAERDPENIDWATDGVEIVLEATGFFAKKEAAEKHLHANGAKKVVITA
                                                                                                                                                                                                 TADORLODAPH - NDIRRARAAVNIVPTTTGAAKAIGLVVPEANGKLNGMSLRVPVLTG
                       PAKEKTIRTVVYNVNHKTISSDDKIİSAASCTTNCLAPLVHVLEKNFGIVYGTMLTVHAY
                                                                                                                                                                                                                                                  SVTELVYTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GAPDH)
                                                                                                                                                              TGDQMILDGPHRGGDLRRARAGAANIVPNSTGAAKAIGLVIPELNGKLDGAAQR
                                                                               TNCLAPMAKALHDAFGIQKGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=168 / BD170;
MEDLINE=89160255; FubMed=2493629;
Viaene A., Dhaese P.;
"Sequence of the glyceraldehyde-3-phosphate dehydrogenase gene Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC 1.2.1.12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2. dependent glyceraldehyde-3-phosphate dehydrogenase)
GAPA OR GAP OR BSU33940.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                            VDGMKLYKVYAWYDNESSYVHQLVRVVSYCAKL
                                                                                                                                                                                                                                                                                                                                    VDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKI
                                                                     PG-GNDVKTVVFNTNHDILDGTETVISGASCT
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MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E., Yoshikawa H., Dancura, Cram-positive bacterium Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 PGGNDVKTVVFNTNHDILD-GTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHAY
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TIGREAMS; TIGRO1534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
INIT_MET 0 0
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                                                                                                                                                                                                                                                                                                                      opposite
                                                                                                                                                                                                                                                                                 Azza S., Dervyn E., Branlant
                                                                                                                 STRAIN=168 / JH642;
MEDLINE=96345629; PubMed=8755892;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
"Cold shock stress-induced proteins in Bacillus subtilis.";
J. Bacteriol. 178:4611-4619(1996).
                                                                                                                                                                                                                                                                                                                "Two glyceraldehyde-3-phosphate dehydrogenases with opposiphysiological roles in a nonphotosynthetic bacterium.";
J. Biol. Chem. 275:14031-14037(2000).

-!- FUNCTION: More active in catabolism.

-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phonomone active in catabolism.

-!- PATHWAY: Second phase of glycolysis; first step.

-!- SUBUNIT: Homotetramer.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SUBCELLULAR LOCATION: Cytoplasmic.
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Pred. No. 1.1e-54,
1; Mismatches 103
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Yoshida K., Yoshikawa H.F., Zumstein "The complete genome sequence of the subtilis.";
                                                                                                                                                                                                                                                               MEDLINE=20261518; PubMed=10799476;
Fillinger S., Boschi-Muller S., Az
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EMBL; Z99121; CAB15399.1; -.
PIR; S02754; DEBSG.
HSSP; P00362; 1GD1.
SubtiList; BG10827; gapA.
InterPro; IPR000173; GAP_dhdro InterPro; IPR006424; GAPDH-I.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
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178 A
35701 MW;
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Similarity 54.5%;
3; Conservative 4
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                                                         Nature 390:249-256(1997)
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334 AA;
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                                                                                                  SEQUENCE OF
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Search completed: May 11, 2004, 16:48:17 Job time : 21 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

May 11, 2004, 16:45:16 ; Search time 46 Seconds (without alignments) 2304.655 Million cell updates/sec Run on:

US-10-650-369-12 1715 1 MVVKVGINGFGRIGRLAFRR......EMSYTAQLVRTLEYFAKIAK 336 score: Title: Perfect

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
5: sp_human:*
5: sp_nammal:*
7: sp_mammal:*
9: sp_organelle:*
9: sp_organelle:*
1: sp_rodent:*
1: sp_rodent:*
2: sp_virus:*
3: sp_virus:*
5: sp_virus:*
5: sp_virus:*
7: sp_bacteriap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	3z£7	Bt	Q9alw2 streptococc	α ω	Ø	Q8gcr7 streptococc	Q97nll streptococc	Q8cwn6 streptococc	Q8khg1 streptococc	Q8dvv3 streptococc	Q8kvu5 streptococc	B	Q915x6 streptococc	Q9ajt7 streptococc	ajt9 st	Q9ajt4 streptococc
SUMMARIES		dī		QBKVU6	Q9ALW2	Q8E3E8	Q8DXS8	Q8GCR7	Q97NL1	QBCWN6	Q8KHG1	Q8DVV3	QBKVUS	Q8VVB9	Q9L5X6	Q9AJT7	Q9AJT9	Q9AJT4
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a	Q83ZF7 PRELIMINARY; PRT; 336 AA.
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DT	MBLrel. 24, Creat
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DE	-P dehyö
GN	GAPC.
SO	Streptococcus dysgalactiae.
၀	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
ပ္ပ	Streptococcus.
XO	NCBI_TaxID=1334;
RN	[1]
RP	A.
æ	Perez-Casal J.F., Bolton A., Song XM., Willson P., Potter A.A.;
RT	ace proteins GapC and Mig of Streptoc
RT	dysgalactiae as protective antigens against mastitis in non-lactating
	COWS.";
	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
	AAP31408.1;
	GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p; IEA
	InterPro; IPR006424; GAPDH-I.
	InterPro; IPR000173; GAP_dhdrogenase.
	Pfam; PF00044; qpdh; 1.
	Pfam: PF02800: grdh C: 1.
	PRINTS: PRO0078: G3PDHDRGNASE.
DR.	TIGREAMS: TIGRO1534: GAPDH-I: 1.
	PROSITE: PS00071: GAPDH: 1.
Š	SEQUENCE 336 AA; 35928 MW; 11828218CF037076 CRC64;
Οm	Query Match Rest Local Similarity 100.0%; Pred No. 5.7e-107;
Σ	16; Conservative 0;
ò	1 MVVKVGINGFGRIGRLÄFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV 60
יר ל	1 MVVKVGTNGFGRTGRTAFFRIONVFGVFVTRINDI,TDPNMI,AHI,IKYDTTOGRFDGTVFV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigens confers protection against heterologous challenge with Streptococcus uberis.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                      TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKG
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase.
Streptococcus uberis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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EMBL; AF421900; AAM73771.1; -.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehy
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh, 2; 1.
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larity 92.9%; Pred. No. 1.8e-100;
Conservative 15; Mismatches 9;
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                                                                                                                                                                                                                        EVDGSQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
KEGGFEVNGNFIKVSAERDPENIDWATDGVEI
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NCBI_TaxID=1349;
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Seifert K.N., Bleiweis A.S., McArthur W.P., Brady L.J.;

"The Group B Streptococcal Surface Antigen Delta is a Glyceraldehyde

3-Phosphate Dehydrogenase.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

C. !- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE

C. !- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE

C. !- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE

REMBL; AF338416; AAK14387.1; -.

REMBL; AF338416; AAK14387.1; -.

ROSP, GO:0004365; F:Glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

ROSP, GO:0016491; F:oxidoreductase activity; IEA.

ROSPONO (173; GAPDH-1.)

RITHERPRO; IPRO00173; GAP_dhdrogenase.

R Pfam; PF00044; gpdh; 1.

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                                                                                                        GSVTELVVTLDKNVSVDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDATQTKVM
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase.
Streptococcus agalactiae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                    TVDGNQLVKVVSWYDNEMSYTAQLVRTLEYFAKIAK
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IGRFAMS; TIGR01534; GAPDH-I; 1.
ROSITE; PS00071; GAPDH; 1.
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Q9ALW2;
01-JUN-2001
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invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766853; CAD47470.1; -.
SagaList; gbs1811; -.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=216495;
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Pred. No. 7.2e-100;
7; Mismatches 10;
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Last annotation
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01-MAR-2003 (TrEMBLrel. 23, Last sequence)
01-OCT-2003 (TrEMBLrel. 25, Last annotat:
Glyceraldehyde 3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=NEM316 / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Ch
Msadek T., Zouine M., Couve E., Lalioui
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l Similarity 92.0%;
309; Conservative 17
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Q8E3E8;
01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; FubMed=12200547;
MEDLINE=22222988; FubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
Fraser C.M.;
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Fraser C.M.;

"Complete genome sequence and comparative genomic analysis of a merging human pathogen, serotype V Streptococcus agalactiae.",

Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).

EMBL; AE014272; AAN00631.1; -..

TIGR; SAG1768; -..

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR00644; GAPDH-I.

R InterPro; IPR006173; GAP_dhdrogenase.

R Ffam; PF02800; gpdh_C; 1.

R PRINTS; PR00078; G3PDHDRGNASE.

TIGRFAMS; TIGR01534; GAPDH-I; 1.

R PROSITE; PS00071; GAPDH-I; 1.
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                                                                                                                                      Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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on update)
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Pred. No. 7.2e-100;
7; Mismatches 10;
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                                                        Last sequence up
                                                                                              Glyceraldehyde 3-phosphate dehydrogenase
GAP OR SAG1768.
                                       Created)
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                                     (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
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est Local Similarity 92...
PRELIMINARY;
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Complete proteome.
SEQUENCE 336 AA;
                                                                                                                                                                                   Streptococcus
NCBI_TaxID=21
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                                                                                                                                                                                                                                                                                           SEQUENCE FACTOR 1.1.

STRAIN=S735;

Brassard J., Gottschalk M., Quessy S.;

Brassard J., Gottschalk M., Quessy S.;

Brassard J., Gottschalk M., Quessy S.;

"Cloning and purification of Streptococcus suis serotype 2 glyceraldehyde-3-phosphate dehydrogenase.";

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY167026; AAN86058.1; -.

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

R Pfam; PF02800; gpdh, 1.

R Pfam; PF02800; gpdh, C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase
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097NL1;
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12).
SP2012 OR GAPDH.
Streptococcus pneumoniae.
Streptococcus pneumoniae.
Streptococcus preumoniae.
Streptococcus preumoniae.
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                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).
Streptococcus suis.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=1307;
                                                                                                                                                                                                                                                                                                                                                 suis serotype
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Pred. No. 5.4e-99
7; Mismatches 13
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TIGRFAMB; TIGR01534; GAPDH-I; 1
PROSITE; PS00071; GAPDH; 1.
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91.1%;
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                          PRELIMINARY;
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SEQUENCE FROM N.A.
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Oxidoreductase.
SEQUENCE 336
                    Q8GCR7;
Q8GCR7;
01-MAR-2003
01-MAR-2003
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Q97NL1
Q8GCR7
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                      SEQUENCE FROM N.A.
STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
MEDLINE=21357209; PubMed=11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC11733;
Bergmann S., Hammerschmidt S.;
Bergmann S., Hammerschmidt S.;
Bergmann S., Hammerschmidt S.;
Bergmann S., Hammerschmidt S.;
Strain S., Hammerschmidt S.;
"Identification of pneumococcal GAPDH as plasmin(ogen)-binding protein.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007490; AAK76079.1; -.
EMBL; AJS05822; CAD44376.1; -.
PIR; F95235; F95235.
HSSP; P00354; 3GPD.
TIGR; SP2012; -.
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GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%; Score 1593.5; DB 16; Lengt larity 92.6%; Pred. No. 7.9e-99; Conservative 12; Mismatches 12; Indels
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PROSITE; PS00071; GAPDH; 1.
Oxidoreductase; Complete proteome SEOUENCE 335 AA; 35856 MW; DA
                                                                                                                                                                                                   pneumoniae.";
Science 293:498-506(2001).
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PROSITE; PS000...,
Oxidoreductase; Comp
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Matches 311; Conser
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Q8CWN6
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=21429245; PubMed=11544234;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Behoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., A LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Morris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Glass J.I., "Genome of the bacterium Streptococcus pneumoniae strain R6.";

"Genome of the bacterium Streptococcus pneumoniae strain R6.";

EMBL; AE008547; AAL00628.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (Phosphorylating)
(EC 1.2.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                  Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO1534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 359 AA; 38763 MW; 61EF0E375B330B60 CRC64;
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12;
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Local Similarity 92.6%;
les 311; Conservative 11
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Oxidoreductase; Composite 359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G98099; G98099
                                                                                                                                                                             Streptococcus.
NCBI_TaxID=171101;
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TAPGGNDVKTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHA
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                                                                                                                                                                                                                                                           "Immunization of dairy cattle with recombinant GapC and chimeric antigens confers protection against heterologous challenge with Streptococcus uberis.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES=S.agalactiae, and S.iniae, STRAIN=ATCC 27541, and 9117;
Fontaine M.C., Perez-Casal J., Song X.-M., Shelford J., Willson
Potter A.A.;
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QBDVV3;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Extracellular glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).
GAPC OR SMU.360.
                                                                                                                                                                                                                                                                                                                                                                                                                            dehydrogenase
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase.
Streptococcus agalactiae, and
Streptococcus iniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=1311, 1346;
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EMBL; AF421899; AAM73773.1; -.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehy
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh, 1.
Pfam; PF02800; gpdh, C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMs; TIGR01534; GAPDH-I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.4%; Score 1584; DB 2;
larity 90.5%; Pred. No. 3.4e-98;
Conservative 19; Mismatches 13;
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304; Conser
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01-OCT-2002 (TrEMBLrel. 22,

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                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=UAL59 / ATCC 700610 / Serotype C;

KREDLINE=22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qia

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.

"Genome sequence of Streptococcus mutans UA159, a cariogenic dent
pathogen.";

Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

EMBL; AE014883; AAN58118.1; -.

GO; GO:00064365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .

GO; GO:0006496; P:glycolysis; IEA.

R GO; GO:0006496; P:glycolysis; IEA.

R InterPro; IPR00644; GAPDH-I.

R InterPro; IPR00644; GAPDH-I.

R Pfam; PF02800; gpdh, 1.

R Pfam; PF02800; gpdh, 1.

R PRINTS; PR00078; G3PDHDRGNASE.
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            Streptococcaceae
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PS00071; GAPDH; 1.
ictase; Complete proteome.
337 AA; 36068 MW; 42BFE20365963C22 CRC64;
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on update)
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                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                         Score 1579.5; DB :
Pred. No. 6.9e-98; 3; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBKVU5
QBKVU5;
QBKVU5;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Glyceraldehyde-3-phosphate dehydrogenase.
Streptococcus parauberis.
Streptococcus parauberis.
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Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales;
Streptococcus.
NCBI_TaxID=1309;
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Best Local Similarity 90.2
Matches 304; Conservative
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Potter A.
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Kuipers O.P., de Vos W.M.;
"Modulation of Glycolysis by Lactose Availability in Streptococcus
thermophilus.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
EMBL; AF442551; AAL35377.1; -.
    recombinant GapC and chimeric; heterologous challenge with
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                                                                                                   -!- SIMILARITY: BELONGS 10 .....

DEHYDROGENASE FAMILY.

EMBL; AF421901; AAM73772.1; -.

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. GO; GO:0006096; P:glycolysis; IEA.

GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF00044; gpdh; 1.

R Pfam; PF02800; gpdh C; 1.

R PRINTS; PR00078; GAPDH-I; 1.

TIGRFAMS; TIGR01534; GAPDH-I; 1.

PROSITE; PS00071; GAPDH; 1.
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                                                                                  databases.
3-PHOSPHATE
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
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Pred. No. 8.6e-98;
5; Mismatches 15
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                                                                                  EMBL/GenBank/DDBJ
THE GLYCERALDEHYDE
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01-MAR-2002 (TrEMBLrel. 20, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Glyceraldehyde-3-phosphate dehydrogenase.
GAPDH.
antigens confers protection against Streptococcus uberis."; Submitted (SEP-2001) to the EMBL/Gen-!- SIMILARITY: BELONGS TO THE GLYCE DEHVNDOORS TO THE GLYCE
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90.8%;
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Best Local Similarity
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NCBI TaxID=13
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QBVVB9;
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         Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-1;
PROSITE; PS00071; GAPDH; 1.
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33968 MW;
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G3PDHDRGNASE
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                                                                                   PROSITE; PS000
Oxidoreductase
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SEQUENCE
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                            dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydrogenase
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae
                                                                                                                                                                                                                                   CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Extracellular glyceraldehyde-3-phosphate dehydrogenase
HSSP, P00354; 3GPD.
GO; GO:0004365; F:glyceraldehyde-3-phosphate dehy
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
Pfam; PF02800; gpdh C; 1.
Prints; PR00078; G3PDHDRGNASE.
TIGRFAMS; TIGR01534; GAPDH-I; 1.
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336
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                                                                                                                                                                                                                                                                  Score 1572; DB 2;
Pred. No. 2.2e-97;
3; Mismatches 15;
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EMBL, AF247678; AAF64063.1; -.

HSSP; P00362; 1GD1.

GO; GO:0004365; F:glyceraldehyde-3-phosphate del

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.
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                                                                                                                                                                                                                                                                    91.7%;
90.2%;
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NCBI TaxID=1
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GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase GO; GO:0006491; F:oxidoreductase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR006424; GAPDH-I.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
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SEQUENCE FROM N.A.
STRAIN=clinical isolate;
Amezaga M.R., Carter P.E., Cash P., McKenzie H.;
Asequence variation in mef(A) and gap genes in M-phenotype erythromycin resistant Streptococcus pneumoniae.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
EMBL; AJ292048; CAC27448.1; -.
HSSP; P00362; IGD1.
                                                                                        Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Last annotation update)
dehydrogenase (EC 1.2.1.12)
                                         Score 1518; DB 2;
Pred. No. 8.4e-94;
4; Mismatches 14;
6FFCC18BB01E91F0
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39E9CC3BEA6F8959 CRC64;

32916 MW;

309 AA;

SEQUENCE

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KTVVFNTNHDILDGTETVISGASCTTNCLAPMAKALHDAFGIQKGLMTTIHAYTGDQMIL 188
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EMBL; AJ292046; CAC27446.1; -.

HSSP; P00362; 1GD1.

GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0006096; P:glycolysis; IEA.

InterPro; IPR006424; GAPDH-I.

InterPro; IPR000173; GAP_dhdrogenase.

Pfam; PF00044; gpdh; 1.

Pfam; PF02800; gpdh C; 1.
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STRAIN=clinical isolate;
Amezaga M.R., Carter P.E., Cash P., McKenzie H.;
"Sequence variation in mef(A) and gap genes in M-phenotype erythromycin resistant Streptococcus pneumoniae.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
                                                                                                                                                      Length
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Streptococcus pneumoniae.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Streptococcus.
                                                                                                  89E45C3BEA6A0528 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
(Fragment).
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.1 Similarity 91.9%; Pred. No. 1.7e-90;
285; Conservative 12; Mismatches 12;
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PROSITE; PS00071;
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                     Gaps
                    1;
DB 2; Length 309;
 ch 85.6%; Score 1467.5; DB 2; Length Similarity 91.6%; Pred. No. 1.9e-90; 284; Conservative 13; Mismatches 12; Indels
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| cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
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SUMMARIES

Description	Sequence 12, Appl Sequence 12, Appli Sequence 12, Appli Sequence 14, Appli Sequence 14, Appl Sequence 22, Appl Sequence 22, Appl Sequence 16, Appl Sequence 16, Appli Sequence 16, Appli	
QI	US-09-878-766A US-09-878-761 US-10-650-369 US-10-134-297 US-10-282-1222 US-09-878-761 US-10-650-369 US-10-650-369 US-10-650-369 US-10-134-297 US-10-134-297 US-09-878-761	
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ALIGNMENTS

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                         Sequence 12, Application US/09878766A
Sequence 12, Application US/09878766A
Patent No. US20020044928A1
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 336
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Sequence 12, Application US/10650369
Sequence 12, Application US/10650369
Publication No. US20040062774A1
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
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; Sequence 4, Application US/09878781
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Pottaine, Michael
; APPLICANT: Pottaine, Michael
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; TITLE OF INVENTION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
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1 Similarity 100.0%; Score 1715; DB 10;
1 Similarity 100.0%; Pred. No. 3.1e-154;
336; Conservative 0; Mismatches 0;
                                                                                                      ORGANISM: Streptococcus dysgalactiae
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Sequence 4, Application US/10134297
Sequence 4, Application US/10134297
Sequence 4, Application US/10134297
Sequence 4, Application US/10134297
GENERAL INFORMATION:
APPLICANT: Belton, Alexandra J.
APPLICANT: Fontaine, Michael
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055.20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US/09/878,766A
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
ORGANISM: Streptococcus dysgalactiae
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US-10-650-369-12
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LENGTH: 336
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APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 335
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                  1 MVVKVGINGFGRIGRLAFRRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDGTVEV
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Publication No. US20030082781A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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APELICANI: Matc.
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APELICANI: Castan, Kari
APELICANI: Castan, Kari
APELICANI: Zayskind, Judith
APELICANI: Zayskind, Judith
APELICANI: Yamamoto, Robert
APELICANI: Sergeth, R.
APELICANI: Source ELITRA 6014
CURRENY PELICATION WINBER: 60/191,078
FILE REPRENCE: ELITRA 6034
CURRENY PELICATION WINBER: 60/191,078
PRIOR PILING DATE: 2000-05-20
PRIOR PELICATION WINBER: 60/200,846
PRIOR PELICATION WINBER: 60/200,935
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PRIOR PELICA
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Mismatches
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; Sequence 74379, Application US/10282122A
; Publication No. US20040029129A1
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5; Conservative
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LICANT: Zamudio, Carlos
LICANT: Zamudio, Carlos
LICANT: Malone, Cheryl
LICANT: Haselbeck, Robert
PLICANT: Ohlsen, Kari
PLICANT: Zyskind, Judith
PLICANT: Trawick, John
PLICANT: Trawick, John
PLICANT: Trawick, John
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                                                       US-09-878-766A-22
; Sequence 22, Application US/09878766A
; Patent No. US20020044928A1
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Perez-Casal, Jose
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CAT7
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INF
FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
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fusion protein
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US-10-650-369-22
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LENGTH: 448
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Sequence 16, Application US/09878766A
Batent No. US20020044928A1
GENERAL INFORMATION:
APPLICANT: Porter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
TITLE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US/09/878,766A
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22.
LENGTH: 448
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OTHER INFORMATION: Description of Artificial Sequence: GapC multiple
OTHER INFORMATION: epitope fusion protein
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Pred. No. 1.7e-148;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEGGFEVNGNFIKVSAERDPE---
                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                / Match
Local Similarity 79.6%;
les 335; Conservative
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; Sequence 8, Application US/09878181
; Publication No. US20030082781A1
; GENERAL INFORMATION;
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AG;
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                        1 MVVKVGINGFGRIGRLAFRIQNVEGVEVTRINDLTDPNMLAHLLKYDTTQGRF
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larity 92.9%; Pred. No. 5.1e-145;
Conservative 15; Mismatches 9;
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Mismatches
           ; TYPE: PRT
; ORGANISM: Streptococcus uberis
US-09-878-766A-16
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312; Conserv
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LENGTH: 336
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Sequence 16, Application US/10650369;
Sequence 16, Application US/10650369;
Publication No. US20040062774A1

GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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                      YTGDQMILDGPHRGGDLRRARAGASNIVPNSTGAAKAIGLVIPELNGKLDGAAQRVPVPT
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Publication No. US20030165524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
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US-10-650-369-16
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ENGTH: 336
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APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Forter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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                    AGAINST
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: protein
APPLICANT: Potter, Andrew A.

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH

TITLE OF INVENTION: STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0055.20

CURRENT APPLICATION NUMBER: US/10/134,297

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0
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larity 92.9%; Pred. No. 5.1e-145;
Conservative 15; Mismatches 9;
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Pred. No. 2.3e-144;
2; Mismatches 14;
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US-10-134-297-8
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ORGANISM: Artificial Sequence
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il Similarity 95.2%;
320; Conservative
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Sequence 14, Application US/09878766A

Sequence 14, Application US/09878766A

Patent No. US20020044928A1

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Potter, OSS

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0
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llarity 91.7%; Pred. No. 1.7e-143;
Conservative 17; Mismatches 11;
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US-09-878-766A-14
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RESULT 15
US-09-878-781-6
; Sequence 6, Application US/09878181
; Publication No. US20030082781A1
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
APPLICANT: Portaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; TITLE OF INVENTION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 6
; LENGTH: 336
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Best Local Similarity 91.7%; Pred. No. 1.7e-143;
Matches 308; Conservative 17; Mismatches 11;
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